

FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGCTGATCC**TG**CACAAGGCGGGCTGCTAGGCCCTC
TGTGCCCCGGCTTGGAAATTGGTCCGGATGGCCAGCTCCGGGATGACCCGCCGGACCCCGCT
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCGC
GTTTGGCCCAGGACGGGGCCATGTGGTCGTCAAGCAGCCGGAAAGCAGCAGAAATGTGGACAG
GCGGTGGCCACGCTGCAAGGGGAGGGCTGAGCGTGACGGGACCGTGCCATGTGGGAA
GGCGGAGGACGGGAGCGGCTGGTGGCACGGCTGTGAAGCTCATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTCAACCCCTTCTTGGAAAGCATAATGGATGTCACTGAGGAGGTG
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAGGCAGTGGTGC
AGAAATGGAGAACGAGGAGGCGCTCAGTGGTATCGTGTCTTCATAGCAGCCTTCAGTC
CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAAACAGCCTTGCTGGCCTGACCAAGACC
CTGGCCATAGAGCTGGCCCAAGGAACATTAGGGTGAACCTGCCTAGCACCTGGACTTATCAA
GAATAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAGCATGAAAGAACCC
TCCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTCCTGTGCTCT
GAAGATGCCAGCTACATCACTGGGAAACAGTGGTGGTGGGAGGAACCCCGTCCCGCCT
CTGAGGACCGGAGACAGCCCACAGGCCAGAGTTGGCTCTAGCTCCTGGTGTGTTCTGC
ATTCAACCACTGGCCTTCCCACCTCTGCTCACCTTACTGTTCACCTCATCAAATCAGTTCT
GCCCTGTGAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCTTACTCGGATTCCCTGCT
GTTGTTGGCCTTGGTAAAGGCCCTCCCTGAGAACACAGGACAGGCCCTGCTGACAAGGCT
GAGTCTACCTGGCAAAGACCAAGATAATTTTCTGGCCACTGGTGAATCTGAGGGTGA
TGGGAGAGAACGGAACTGGAGTGGAAAGGAGCAGAGTTGCAAATTAAACAGCTTGCAAATGAGG
TGCAAATAAAATGCAGATGATTGCGCCGGCTTGAAAAAA

FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672
><subunit 1 of 1, 278 aa, 1 stop
><MW: 29537, pI: 8.97, NX(S/T): 1
MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVVS
SRKQQNVDQAVATLQGEGLSVTGTVCVGKAEDRERLVTAVKLHGGIDILVSNAAVNPFFG
SIMDVTEEVWDKTLDINVKAPALMTKAVVPEMEKRGGSVVIVSSIAAFSPSPGFSPYNVSK
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC
AGIVSFLCSEDASYITGETVVVGGGTPSRL
```

Important features of the protein:

Signal peptide:

amino acids 1-15

N-glycosylation site.

amino acids 183-186

N-myristoylation sites.

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

Microbodies C-terminal targeting signal.

amino acids 276-278

FIGURE 3

GGCGCCCTGAGCTCCGCCTCCGGGCCGATA CGG CTCGAGAGGCCCTCCGTGAGGACCGAGCGCG
CAGGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCCCTGCAGAACCCAGGTGGC
GCGGCTGGAGGAGGAACCGAGACTTCCTGGCTCGCTGGAGGACGCCATGGAGCAGTACAAACTGC
AGAGCGACCCGCTGGCTGAGCAGCAGGAGGAGATGGTGAACCTGGCGCTGGGGCTGGGTTAGAGCTGGTGC
CCAGGGCTGGGGGGCTCGGGCTCTGAATGGCTGCCTCCGGGCTTGTGCCTCGACCCATAC
AGCCCCCTGGGGGTGCCCCAGCCCATGTGCTGGCATGGTGCCTGCCTGCCTCCCTGGAGATG
AAGTTGGCTCTGAGCAGAGGGGAGACGAGCTGAAATGCGAGGGGGCTGGAGCTGAAGTGTGACT
GAGGTGAACAGGCTGGGAAGTGGCTCTGAGCTCAGAGGAGGAAGAGGAGGAGGAGGAGGCC
CAGCGGACCTTACACCTGGCAGAAATAGGATCAGCAACTGAGCTCAGAGGGCGGGGACGCCAG
GGAGTCTGCCAGAGAGGAAGGGCCCAGAGCTTGGCTTGGAGGATGGATGCAGCATTCCAGGGTCC
AGAGCAGTTGGTGGAGCAAGGCCAGGTTAGGGCCAGGGCTCCACAGCCTCAGAGTG
GGGGCTGGCCGGCCAGAGCAAGATCCGGAGCTGGCTATCAACATCGCAGTAAGGGAGGCTTA
TTGGCAGACTGTGTCGCCAGGAAAGGACCTCAGGGCTGAAAGGCCAGCACAGCCAGCTATCGG
GAGCTGGAGCAGGAGGAGCAGCAGGTGCGGGCGAGCTGAGTGAAGGCCAGAGGAGCTGCGGGAGCT
CGAGGCAAGAGGACTCCAGATGTGGCAGCGCCTGGCTCCAGGAAGTCCCGAGGGGGTCTG
CGGGCCAGAGGCCAGGTGCTGAGGAGAAGAGCAGGCTAGGGCAGCAACGGCTCTGTGGTCACTGTG
GCCAGAGTGAGAAGCGACTCAGGAGCTCAGGCCAGCTGGCAGCTCATGGCAGCACAGGGACA
GCTGCAGAGGCCCTCGCAGGAGACGGAGCAGAAGCGGCCCTGGAGGAGAAATGAGCAAGGGC
AGCACCGCTCAAGGAGCTGGAGCTGAAGCATGCCAACAGCAGAAAGATCTGAGAAGATTAAGGGAA
GAGATCGGCCCTTCAGAGGAAGAGGCCAGTGGCAGCAACGGCTCTGTGGTCAAGCAGCA
GCAGAAGATTGAGGAGCAGAAAGTGGCTGGACCCAGGAGATGGAGAAGGGTGTACAGCAGGCCGGG
CGCTGGAGGAGCTGGGGAGGAGCTCCACAAAGCGGGAGGACATCTGGCCAAGAAGGAGGCCCTGATG
CAGGAGAAGACGGGGCTGGAGAGCAAGGCCCTGAGATCCAGGCCAGGGCTCTCAACAGGACATCTGG
AGTGTCCAGGGCTGAGCACCTGGAGAAGGAGCTGTCGGAGAAGAGCGGCCAGCTGCCAGGGCA
GCGCCAGAGCCAGCAGCAGATCCGGGGAGATCAGACAGCCTGCCAGGAGAAGGACTCGCTGCTC
AAGCACGCCCTGGAGATCGAGGCAAGCTGAGGGAGGACTCTGTGTCCTCCAGGAGGAGGCC
GCTGTTCAGGGTGTGGAGCTGGGAGGAGCTGGCTGGAGGAGATGGACCCCTGGAGGAGGAGGCC
CATGGCCAGGGGGCTCTGGGCTCAGCCTCGTGTGTCCTCCAGTGGAGATGAACCTCATGGC
AAGCTCAGCTACCTCTCATCTCAGAGACCAGAGGCCCTCTCTGCAAGTATTTGACAAGGTGGTGC
GCTCCAGAGGAGGAGCACCACAGCAGATGGCTCTCTGCAAGGAGCTGGAGCAGCTGGAGGAGCAGC
AGAGGTGGTGTACTGGTGGAGGTTGGCCCTGGAGGGCAGCAGCTGGAGGAGATGGACCCGCACTGACC
CTGCAGCAGAAGGAGCACGAGCAAGCATCAGCTGCTCTGGCAGAGCTGAGACCACTCGTG
AGGGTAGCAGACAGCAGGAGGAGCTATGAGGCCGGATTCAAGCTCTGGAGAAGGAACCTGGCCGTT
ACATGTGGATAAACAGGAGATAACAGAGCTGGGGCTGTGAAACGCTGTAAGGCCACAGCAGGG
GGGGAGAAGAGGAGGAGCTGTGCTGGAGGGCAGACAGGCTCTGGAAATGAAGATGAGCTCCACCTGGC
ACCCGAGCTCTCTGGCTGCCCCCTCACTGAGGGGCCCGCAGCCGGAGGAGACGCCGGACT
TGGTCCACGCTCGTGTACCTGGACTGGAAACGCTGAGGCTGTGTGGTGGAGGAGCAGGGTCCCC
GAGGAACCTGAGGAGCAGGGAGGGCTGAGGCCCTGTGGGGGGGTGCTTCTGTGGGTGAGGGCAGG
CTGGCCCTGGAACTTGGGCTTTGTCAAGGCCGGGGAACTGCGAGGAGCCGGGGATGAA
TTGATGTCCGGAAAACCCCTGTAAAGCCTCTGGGGCAGACCCCTGCTTGGGGAGACTCCGAGCCT
GCTGAAAGGGCAGCTGCTGTGTTCTGTGAAAGGGCAGTCCCTAACCCACCCCTAAATCAGG
CCCTCATCTGACCCCTCACTGGGATCAACAAATTGGGCAATGGCCAAAAGAAGACTGGACCCCTCATT
AAACAAATAATGCAAATTCCACCACTACTTCCATGAAGCTGTGGTACCCATTGGCCCTTGTG
TCTTGCTGAGATCTCAGGACAATTCTGGTTTCAGCGTAAATGGATGTGCTTGTAGTTCAAGGGTTG
GCCAAGAATCATCAGGAAAGGGTCGCTGGCAACCGAGTTGGTTAAATGTCCTTATGTATAGGG
GAAACTGGGAGACTTGTAGGATCTTAAAAAACCTTAAATAAAAAAAATCTTGAAGGGAC

FIGURE 4

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465
<subunit 1 of 1, 830 aa, 1 stop
<MW: 95029, pI: 8.26, NX(S/T): 2
MEQYKLQSDRLREQQEEMVELRLRLELVLRPGWGGRLRNGLPPGSFVPRPHTAPLGGAHAV
LGMVPPACLPGDEVGSERGEGVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEPPRRTL
HLRRNRISNCSQRAGARPGSLPERKGPELCLEELDAAIPGSRAVGGSKARVQARQVPPATAS
EWRLAQAAQQKIRELAINIRMKEELIGELVRTGAAQALNRQHSQRIRELEQEAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQLKEKKQATERLVSLSAQSEKRLQE
LERNVQLMRQQGQLQRLREETEQKRRLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA
AFQRKRRSGNSNGSVSLEQQKIEEQKWKLDQEMEKVLQQRRALEELGEELHKRAILAKKE
ALMQEKTGLESKRLRSSLQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAQSQQQIRGEIDS
LRQEKDSSLKQRLIEDGKLQRQGSLLSPEEERTLFQLDEAIEALDAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMALKSYLSSETRALLCKYFDKVVTLREEQHQQQIAFSELEMQLEEQQR
LVYWLVALERQRLEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGLADSRRQYEARIQALEK
ELGRYMWINQELKQKLGGNAVGHSGRGKRSCLCSEGQRQAPGNEDELHLAPELLWLSPLTEG
APRTTRETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGAEAGLPWNFG
PLSKPRRELRRASPGMIDVRKNPL
```

Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

FIGURE 5

ATTCTCCTAGAGCATCTTGGAAAGC**ATG**AGGCCACGATGCTGCATCTGGCTTGTCTGCT
GGATAACAGTCTTCTCTCCAGTGTCAAAGGAACATACAGACGCCCTGTTGGCTCAGGA
CTGTGGCTGTGCCAGCCGACACCAGGTGTGGAACAAAGATCTACAACCCCTCAGAGCAGTG
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT
TCTGGCCCTGCTTGAGCTCTGCTGTCCGAGTCTTTGGCCCCAGCAGAAGTTCTTG
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACTTATCTCCCATCTCCGGAGCTGTAC
CAGGAACAGGAGGCACGTCCGTACCCAT**AAAAA**ACCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGGAGAAGAGAGCAAGCAGCTGGACATCGGAGACTACAGTTGAACCTCGGAGAGAAGCA
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTGGAGAGGAGGCCAGCTGGGATGGC
CAGACTTCAGGGGAAGAATGCCCTCTGCTTCATCCCCTTCCAGCTCCCCTCCCGCTGAG
AGCCACTTTCATCGGCAATAAAATCCCCACATTACCATCT

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700
><subunit 1 of 1, 125 aa, 1 stop
><MW: 14198, PI: 9.01, NX(S/T): 1
MRPRCCILALVCWITVFLLQCSKGTTDAPVGSGLWLQPTPRCGNKIYNPSEQCCYDDAILS
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRLVLMKSQCHLSPISRSCTRNRRHVLYP
```

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

FIGURE 7

CCCCACGCGTCCGCCACCGCTCCGGTGCACACTCGCGCAGCGCCGGCCGCTCCGGCTCTCT
TTTCCCTCCGACGCCACGGCTGCCAGACATTCCGGCTGCCGGGCTGGAGAGCTCCCG
AACCCTCCGGAGAGGAGCGAGGCCAGGGTGGCCCCGGGCGCTGGCTCG
GAGAAGCGGGGACGAGGCCAGGGATGAGCGACTGAGGGCGACGCCGGACTGACCGAGTT
GGGGCGCGACTACCGGAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCG
GTGTGCGCCAGGCCAGGGAGCGCGCAGGTGGGCTGGGCTGTTAGTGGTCCGCCAACGCC
TCGCCGGCCGCCAGGATGGCGCTGGCAACCCGGCCCGCCGCGCTGCTACCCCTG
CGCCCGCTGCGAGCCCGCGTCCGGCCCGCCCTGCGCTCATGGACGCCGGCTCCGGCTG
GCCGCCGCCGCCGCCGGGCTGTGAATGCACTGCCCTCGGCCGCTCCCCGCCGCC
GCCGCCGCCAGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA
GTTCCCTCTGGTACCTGCTGCCGTGGCTCTGTGAGTCGAGCCTCCGAG
AAGCTGGCCCAAGGCCACAGAGCAGCGGGCCAGGAGAAGCGTGAGCACGCCACTGGGACGG
CCCGGGGGGGTGAACGAGCTCGGCCGCCGGCAGGGAGCAGGGCGCAGCGGGGGACT
GGAAGAGCAAGAGCGGCCGTGGCGCCGGCGTGAGCGTGGAGCAAGCTGAAGCAGGCC
TGGGCTCCAGGGCGGGGGCGCAAGGCCGGGATCTGAGGTCCGCCCGGGGACAC
CCCGCAGGCCAGGCCCTGGCCGAGCCGCCAGGACCGATTGGCCCGAAGTCCGCC
CGCCGAGGCCACCGAGGAGTACGTGACCCGACTACCGTGGCAAGGGCTGCGTGGACAG
AGCGGCTTCGTGACCGATCGGGAGAAGTTCGCCGGGCCCTCGGCTGCCGTGCT
GTGCAACGAGGAGGGGCCGTGTGCGCGCAGCCGAGTGCCTGGAGGCTGCACCCGCTGCA
TCCACGTGCAACGAGCCAGTGTGCTGCCGAGTCAAGGAGAGGAAGAACTACTGCGAGTT
CGGGCAAGACCTATCAGACTTGGAGGAGTCTGTGGTCTCCATGCGAGAGGTGTCGCTG
TGAAGCCAAGGGTGAGGTGCTATGCAAGTGTGAGCGTGTCCCCAGACGGAGTGTGGACC
CTGTGTACGGAGCCTGATCAGTGTGCTCCATCTGCAAAATGGTCAAAGTGTGCTGGAGAA
ACCGCGGTGATCCCTGCTGGCAGAGAAAGTGAAGACTGACGAGTGCACCATATGCCACTGTAC
TTATGAGGAAGGCACATGGAGAATCGAGCGCAGGCCATGTGCAAGGAGACATGAATGCAAGC
AAATGTAGACGCTCCAGAACACAAACTCTGACTTTCTAGAACATTTACTGATGTGAA
CATTCTAGATGACTCTGGAACTATCAGTCAAAGAAGACTTTGATGAGGAATAATGGAAAA
TTGTTGGTACTTTCTTCTGTATAACAGTTACTACAACAGAAGGAATGGATATATTC
AAAACATCAACAAGAACCTTGGCATAAAATCCTCTCTAAATAAATGTGCTATTTCACAG
TAAGTACACAAAAGTACACTATTATATCAAATGTATTCTATAATCCCTCATTAGAGAG
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AAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818
><subunit 1 of 1, 325 aa, 1 stop
><MW: 35296, pI: 5.37, NX(S/T): 0
MPSSTAMAVGALSSSLVTCLMVALCSPSIPLEKLAQAPEQPGQEKRREHATRDGPGRVNEL
GRPARDEGGSGRDWKSRSRGLLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTPQAEALA
AAAQDAIGPELAPTPEPPEEYVYPDYRGKGCVDESGFVYAIIGEKFAPGPSACPCLCTEEGPL
CAQPECPRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCEANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEEGTWR
IERQAMCTRHECRQM
```

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

FIGURE 9

CAGCCACAGACGGGTCATAGGGCGGTATTACTGCTGGCCCTCCTGGGTTCATCCTCCCCAC
TGCCAGGAGTGCAGGCCCTGCTCTGCCAGTTGGGACAGTTCACTGAGCATGTGTGGAAGGTGTCC
GACCTACCCCGCAATGGACCCCTAAGAACACCAGCTGCACAGCGCTTGGGTTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGGCTGGTGCTCTCCAAGGGTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACGGATGGGCCCCGCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACCTCCCTCCCGCT
TTGGGCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCGGAGGGGACAACAGAAGAGATCTGCCCAAGGGACACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAATTGGGCCGTGGGTATGACTGAGA
ACTGCAATAGGAAGATTTCTGACCTGTATCGGGGACCAACATTATGACACACGGAAAC
TTGGCTCAAGAACCCACTGATGGACCACATCGAATACCGAGATGTGAGGTGGGCAGGT
GTGTCAGGAGACGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGACAAAG
GCTGCAGCACTGTTGGGCTCAAATTCCCAGAAGACCAACATCCACTCAGCCCCCTGGG
GTGCTTGTGCCCTCTATACCCACTTCTGCTCTGCCACCTGTGCAATAGTGCCAGCAG
CAGCGTTCTGCTGAACCTCCCTCCCTCAAGCTGCCCTGTCCCAGGAGACCGGAGTGT
CTACCTGTGTCAGCCCCCTGGAACCTGTTCAAGTGGCTCCCTGGGAATGACCTGCCAGG
GGGCCACTCATGTTATGATGGTACATTCTCAGGAGGTGGCTGTCCACCAAAAT
GAGCATTAGGGCTGCGTGGCCCAACCTTCAGCTTCTGTGAACCACACCAGACAAATCG
GGATCTTCTGCGCGTGAGAAGCGTGTGAGCTGAGCTCTGCCCTCAGCATGAGGGAGGT
GGGGCTGAGGGCTGGAGTCTCACTGGGGGTGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGGTTGCCCTCCTGCTAACTTATTACCCACGATTCTCACCGCTGCTGA
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTGGACACCAGATTCTTC
CCATTCTGTCATGAATCATCTTCCCCACACAACTCATTCTATCTACTCACCTAACAGCA
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GCTGCATGTATCTGATAATACAGACCCCTGTCCCTTCA

FIGURE 10

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ESGPQVSLVLSKGCTEAKDQEPRVTEHMRGPGLSISYTFVCRQEDPCNNLVNSLPLWAPQP
PADPGSLRPCVCLSMEGCLEGTTEECPKGTTCHYDGLLRLRGGGIFSNLRVQGCPQPGCN
LLNGTQEIGPGVGMTECNRKDFLTCHRGTTIMTHGNLQAQEPTDWTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGKGCTVGAQNSQKTTIHSAPPGLVASYTHFCSSDLCNSASSSVLLN
SLPPQAAPVPGDRQCPCTCVPGLTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
VAQPSSFLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWGVVCPSC

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristoylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

FIGURE 11

CGACGATGCTACGCGCCGGCTGCCCTCCTCCGGACCTCCGTAGCGCTGCCGGCCCTG
GCTCGGGCGCTGCTCTCGCCTGCGCTGCTCTCTAGAGCGAGGGACCCGGTGGC
CTCGTCGCTCAGCCCCATTTCGGCACCAAGACTCGCTACGAGGATGTCACCCCGTCTAT
TGTGGGCCCCGAGGCTCGTGGCGGACCCCTGAGCTGCTGGAGGGACCTGCACCCGGT
CAGCTGGTCGCCCTATTGCGCACCGCACCCGCTACCCACGGTCAAACAGATCCGAAAGCT
GAGGCAGCTGCACGGGTTGCTGCAGGGCCGGGGTCAGGGATGGCGGGCTAGTAGTACCG
GCAGCCGCGACCTGGTGCAGCGCTGGCGACTGGCTTTGTTAAGCAGGGACTGGATGGAC
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGGCACAGCTGGCGCTGCGGCTCATCACCAGTCCAAGC
ACCGCTGCATGGATAGCAGCGCCGCCCTCTCGCAGGGCTGTGGCAGCACTACCAACCTGGC
TTGCGCCGGCCGGACGCTCCAGATTTGGAGTGGACCTTCAACAGTTAATGATAAACTAAT
GAGATTTTGATCACTGTGAGAAGTTTAACTGAAGTAGAAAAAAATGCTACAGCTCTT
ATCACGTGGAAGCCTTAAACTGGACCCAGAAATGCAACATTTAAAAAAAGTGCAGCT
ACTTTGCAAGTGCAGTAAATGATTTAAATGCAAGATTAATTCAAGTAGCCTTTCACCTG
TTCAATTGACCTGGCAATTAAAGGTGTTAAATCTCTTGGTGTGATGTTTGACATAGAT
ATGCAAAAGTATTAGAATTTAAATGATCTGAACAAATTTGGAAAAGAGGATATGGTAT
ACTATTAAACAGTCAGTCAGCTGCACCTTGGTTCAGGATATTTCAAGCACTTGGACAAAGC
ATTTGAGACAGAAACAAAGGCTCAGCAATTCTCTCCAGTCATCCTCCAGTTGGTCA
CAGAGACTCTCTTCACTGTTCTCATGGCTACTTCAAAGACAAGAACCCCTAAC
GCGTACAATTACAAAAACAAATGCATCGGAAGTCCGAAGTGGCTCATGGTACCTTATGC
CTCGAACCTGATATTGTCCTTACACTGTGAAAATGCTAAGACTCTAAAGAACATTC
GAGTGCAGATGTTAAATGAAAGGTTACCTTGGCTTACTCACAAGAAACTGTTCA
TTTATGAAGATCTGAAGAACCACTAACAGGACATCTTCAGAGTGTCAAACCAAGTGAAGA
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AATTCTTAGGAATCTGCAATGAGTGAATTACATGCTGTAAATGGTAGGAATTCTTGATT
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AGATTTGTTCTGCAAGTCTCTCTCTTCTCAGGTAGGACAGCTAGCATTCTTAAATC
AGGAATATTGTGGTAAGCTGGAGTATCACTCTGGAAAGAAAGTAACATCTCCAGATGAGAA
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TGAAAATAATATTGGTATTATGAAATTGAACTTTCAATAATTCAACACTTGGAAAGTGC
TTTACTCTAGGAAGTCTCAAAGACCATCTTAAATTATTATGTTGGACAATTGAAAC
AAGTCAGATAGTTAGAAATGCAAGTTTCAATCATTGCTTAGCTAACTTTTCAATTCTGT
CACTGGCTTCGATTTCATTTCTTCAATTATGAAATGTTCTTGGTTGTTGATT
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FIGURE 12

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GPEAPW RDPELLEGTC T P V Q L V A L I R H G T R Y P T V K Q I R K L R Q L H G L L Q A R G S R D G G A S S T G S
RDLGAA LADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFIQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVATLQVPVN DLNADLIQVAFFTCSDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKEPLTAYNKKQMRKFRSGLIVPVYASNLIFVLYHCENAKTPKEQFRV
QMLLNEKVLPLAYSQETVSFYEDILKNHYKDILQSCQTSEECELARANSTSDEL

Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

FIGURE 13

GGGACTACAAGCCGCGCCGCGCTGCCGCTGCCCTCAGCAACCCCTGCACATGGCGCTGAGGCCGCCACCGCAG
TCCGGCTCTGGCTCGGCTGCCCTGACTTCTCTCTGCTGCTGCTTCAAGGGCTGCCCTGATAGGGCTGTAATC
TCAAATCCAGAACATCGAACCCAGTGTGACAGGAATTGAAAGTGTGAACTGTGCTTCCATATTACGGATTGCG
AGACAGAAGTGGCCAGGATCGAGTGGAAAGAAAATTCAAGATGAAACAAACACATATGTGTTTTGAAACAAAAA
TTCAAGGGAGACTTGGCCGCTCGCAGAAATTACTGGGGAAAGACATCCCTGAAGAATCTGGAATTGTGACCGAGAG
ACTCAGCCCTTATCGCTGTGAGGTGCTGCTGCAAATGACCGAAGGAAATTGTGAGATTGTGATCGAGTTAA
CTGTCAGAACAGTGAAGCCAGTGACCCCTGCTGTAGAGTGCAGGAAAGGGCTGACAGTGGCAAGATGCCAACACTGC
ACTGCCAGGAGAGTGGAGGGCCACGGGCTCACTACAGTGTGATCGCAATGTGATTACACTGCCACGGATT
CCAGAGCCAATCCCAAGATTTCGCAATTCTCTTCCACTTAAACTCTGAAACAGGCACTTTGGTGTCACTGCTG
TTCAAAAGGACACTGCGCAACTACTGCACTGCTTCCAAATGACCGCAGGCTCAGCCAGGTGAGGAGCAG
AGATGGAGACTTGTGACCCATGGGGAAATTGGGGGGTTCTGGTTGTCTTGTGACTGCCCTGTA
TCACGTTGGCAGTCGCTGTGACAGACGTTGCTACTTCATCAACAAATAACGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCCAGATGGGAAACTACATCCGCACTGACGAGGAGGGCAGACTTCAGACAACTGATCATGTTG
TGATCTGAACCCGGCGCTGTGGTGAAGGGCCACAGAGCGCACCTGCAACATACCTCTGCTGAAACTCTGTCAA
GGCAGCGAGAGCTGATGCACTGGACAGAGCTGAGACACTTCAAGAGCTTTTGCTTGGCCAAGTTGACCA
CTACTCTTCTACTAAACAGGCCATGAATAGAAGAAATTCTCAAGATGGACCCGGTAAACATGGGGAA
GGAGGCAAATTGGTGTGCTTCACTGAGTTGGCTCTTCAAGTGTGCTTGGCTGATTCCCGCATGAGTATTAG
GTGATCTTAAAGAGTTGTCTCAGTAAACGCCGTGCTGGGCCCTGTGAAGCCAGCATGTTACCAACTGGTGT
CAGCGACCCAGCACGACCATCTGAGATGGCAGGGTGTGGCAAGCAGCACCGCAGTCCGGGGGAAACCA
GAAAAGCTCTTACACAGCAGCTTACATCTGAGCTTGGAGAGCTTTTGATGCACTTTGTA
GTTAAAACACAGGCTTCTGAGTGTGCTTGGAGAGGATCTGGCTGAGGAACTCTGCTTGGTCAACAGGGTGTCAAGGATTA
GTTAAAATGGTGTCTGGAGAGGATCTGGCTGAGGAACTCTGCTTGGTCAACAGGGTGTCAAGGATTA
ACCTCTGCTTCTGGCTTCAAGTGTGACTTCAAAATGCTTCAAGTGTGCTTCTGTTTATTTTAAATTAAATT
TACATCTAAATTCTGCAAGAGTGTATTGATTGAAAGAAAATTCTATTAAACTGTAAATATAATTGT
CATACATGTAAATACCTATTCTTAAATTAAAAGTCAACTTAAAGTGAAGTCAAGGCTACTATGTAAAT
TGGAAAATATCAAAATTAAGTATTCTACCAAGGAACCTCTCTGAGTTTACTGTGATGTTCTTCT
CACACAAGTTTACGCCCTTCAAAAGGAACTCATACTGTCTACATCGACACCATGTTCTAGGAACCTT
TAAATTCAGTGGAGCAACTGTGATCTCTTCAAAAGAAGAACCTCTCAGGTTGACTTGTGAACT
GCCCTCTCTGGAGATGAGTACAGGACTCTGCTACCCAGGGCCACCGAAGCCCTCAGATGTACATCACAGATG
CCAGTCAGCTCTGGGGTGTGCCAGGGCCCCCGCTTAGCTACTGTGCTGCCGTGCTGCCAGGAGGCC
GCCATCTTCTGGCCCTGGACTGGCTGTGCTCAGGCTTACTGCTGCTGCCCTGCTCATCCAGCACAGC
TCTCAGGTTGGGACTCGAGGGACACTGGTGTCTTCCATGAGCTGGCCACGTTGGCTCTGTAA
TTGGTTATGGTGTGCTCACAAATAGGGCCCTTACAGTATTGTTAAGTTGTTAAATTATTGTT
AAAGATGGCTTCAAGGCAAACGGCAATTCAAGTGTCTGCAAGTAAACATTTTAAAAGAAAATGGAT
CCCACCTGTTCTTCTGGCCACAGAGAACCCAGAGCCACAGGCTCTGTCGCAATTCAAAACACCATGAT
GGAGTGGCCGCCAGTCAGGCCCTTAAAGAACGTCAGGTGGAGCAGCAGGTGAAGGCCCTGGGGAGAAAAG
TGAAAAGGCTGTAATCAAAAGTGTCTTCAATTGATGCTTAAATTCTGATCTTAAATTCTCATCCGGAGAGACTCTCC
TGTGTTGGGAGCATTAGCAACATCCTGAGGCTGTGTTCTCAAGAGCAGGTGTTCTCAGGCTCAATGCC
GCCGCTGAGACTCAGGACTGAGTGTGTAAGCAAGGAGCTGCTGAGAAGGAGCACTCCTACTGTGCTG
GAATGGCTCTCACTCACCCTGCTTCACTGCTTCAAGTGGCTTAAATTGACAGCTT
AATTGACATACATGAGACTGTGACTTATTGTTAGTTATGTGAACACTTGGCCAGGCCCTGGAGAGGCA
GGAAAATGCTCAGCAGTGGCTACTGCTCCCTGGTGTGCTGCACTGCTGATCTGGATGCTTAGCATGCAAGTTC
CTCTCCATCTGGCCACCTTGTAGAGGGATGGCTCCACCCCTCAGGGTTGGGATTCTACGCTCAGGCC
TCTTGGTTGTCTAGTGTGACTGGCTTATGCCCCCTCTTCTTATACCCCTAAACCTCTACACTGTGCA
TGGGAACCGAGTGTGAAAGTGAAGAGAAGTGAAGTGAAGTCTGGAAAGTGAAGTCTGGCTATAACTGAGACTGAG
CGGAAAAGGAATACTCTGTATTTTAAGATGATGTGACTCAAGACTCGAGGGCGATACAGGGTGTGATTCT
GCCCTTGGATGGATGTGCTGACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTCAAAAACCCA

FIGURE 14

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRRLCARLPDFLLLLFRGCLIGAVNLKSSNRTPVVQEFESELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIA SNDAGSARCEEQEMEVYDLNIGGIIGG
VLLVVLAVLALITLGI CCAYRRGYF INNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

FIGURE 15

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

MHILVVHAMVILLTGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLLPDWLKLRM
IRSEVLRLVDAALQDLEPQQQLLLFVQSGIPVSSMSKLLQFLDQAVAHDPPQTLEQNIMDKNY
MAHLVEVQHERGASGGQTFFHSLLTASLPPRRDSTEAPPKPKSSPEQPIGOGIRIVGTLRVLG
PEDDLAGMFLQIFPPLSPDPRWQSSSPRVALALQQALGQELARVVQGSPEVPGITVRVLQAL
ATLSSPHGGALVMSMHSRHFACPLLRQLCQYRCPQDTGFSSLFLKVLLQMLQWLDSPG
VECGPLRAQLRMLASQASAGRRLSDVRRGLLRLAEALAFRQDLEVVSVSTVRAVIATLRSGEQ
CSVEPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASPFPACKPVVVVSSLLQEEPLA
GKGPAGDGSLEAVRGLPGSGLLWDLWEMLDPEVVSSCPDLQLRLLFSRRKGKGQAVQPSFR
PYLLTFLTHQSSWPTLHQCIRVLLGKSREREQRFDPSASLDLWACIHVPRIWQGRDQRTPQKR
REELVLRVQGPTELISLVELILAEAEATRSQDGDTAACSLIQARLPLLLSCCGDDESVRKVTE
HLSGCIOQQWGSVLRGRRCDLLLQLYLQRPELRVPVPEVLLHSEGAASSSVCKLDGLIHRFI
TLLADTSDSRALENRGADASMACRKLAVAHPLLRLRHPMIAALLHGRTHLNFQEFRQQNHL
SCFLHVGLLELLQPHVFRSEHQGALWDCLLSFIRLLLNRYKSSRHLAAFINKFVQFIHKYI
TYNAPAAISFLQKHADPLHDLSFDNSDLVMLKSLLAGLSPSRDDRTDRLGDEESEESSAG
SLPLVSVSLFTPLTAEMAPYMKRLSRGQTVEDLLEVLSIDEMSSRRPEILSFTNSTNLQRL
MSSAEECCRNLIAFLSALRSMQNSPSTAAAFLPTFMYCLGSQDFEVVQTALRNLPEYALLCQE
HAAVLLHRAFLVGMYQGMDPSAQISEALRILHMEAVM

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,

665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

FIGURE 17

CCGGGCCATGCAGCCTCGGCCCCCGGGCGCCGCCGCACCCGAGGAGATGAGGCTCCGC
AAAGGCACCTTCTGACGCTGCTCTTCTGCTGTGCGCTTCTCTCGCTGTCTGGTA
CGCGGCACCTAGCGGCCAGAAAGGCACGTTGTGGACGTTTACACAGCGGGAGTTCTGGCG
TGCAGCGATCGGTTGCACCGCAGCTGAGCAGGAGACCTCAAGCGCTCCAAGGAGCTAACCTG
GTGCTGGACAGATAAAGAGGGCGCTGTCAAGAAAGGCAGGGCTGCGAGACGGAGACGGCAA
TCGCACCTGGGGCGCTAACAGAGGACCCCGATTGAAGCCGTGGAACGGCTCACACCGGC
ACGTGCTGACCTGCCAACCGCTTCTCATACCTGCACACCTGCTGGCCAAGGAGACGAGT
CTGCAGGCCGCGGTGCGCGTGGGCCAGGGCGCACCGGAGTGTGCGTGGTGTGGCATCCC
GAGCGTGGCGCGAGGTGCACTCGTACCTGACTGACACTCTGACTCGCTCATCTCGAGC
TGAGCCCAGGAGAAGGAGGACTCGGTACATCGTGTGCTGATCGCCGAGACTGACTCACAG
TACACTTCCGCAGTGCAGAGAACATCAAGGGCTTGTTCACCGAGATCCATCTGGGCT
CCTGGAGGTATCTCACCTCCCCCCTACTCATCCCTGACTTCTCCGCCCTGGAGACTCT
TTGGGGACCCAAGGAGAGTCAAGTGGAGGACAAACAGAACCTGATTACTGTTCTC
ATGATGTACCGCAGTCAAAGGCATCTACTAGTCAGCTGGAGGATGACATCGTGGCAA
GCCAACTACTGAGCACCATGAAGAACATTGCACTGCAGCAGCCTTCAAGGAGACTGATGA
TCCCTGGAGTTCTCCAGCTGGGCTTCATTGGTAAGATGTTCAAGTGCCTGGACCTGAGCTG
ATTGTAGAGTTCATCTCATGGTCTACCGGGAACAGGCAAGGGCTGACTGGCTCCGGACCATAT
TCTGTGGGTGAAAGTCTGCAACCCCCAGAAGGATGCGAAGCACTGTGACCCGAGAACGCCA
ACCTCGGGATCGCTTCAACCGTCCCCCTTCAGCACGTGGGACTCACTCTCGTGGCT
GGCAAGATCCAGAAACTGAAGGACAAAGACTTTGGAAAGCAGGCGCTGCGGAAGGACCATGT
GAACCCGCCAGCAGAGGTGAGCAGGCCAGCTGAAGAACATCACAGCACCTCCGGAGAAAG
CCTACCTGCGAGGGACTCTTCTGGGCTTCACCCCTGCGCGGGGGACTTCATCCGCTTC
CGCTTCTCCAACCTCTAGACTGGAGGGTTCTCTTCCGAGTGGGAACATCGACCAACCC
GGAGGACAAGCTTCAACACGTCGTGGAGGTGCTGCCCTCGACAACCCCTAGTCAGACA
AGGAGGCCCTGAGGAGGGCCGACCCGCCACCTCCGGTACCCCTGGAGGCCAGGCTAC
CTCCAGATCGGCTCTTACAAAGGGAGTGGCAGAGGGAGGGTGGACCCAGCCTCGGCC
TCTGGAGACACTGCGCTCTCGATCCAGACGGACTCCCTGTGTGGGTGATTCTGAGCAGA
TCTTCTGAAAAGGCCACTAAGTCAGCTGGGCTTCTGAGGGTACCTGTGCCAGCCCTGAA
GCCACATTCTGGGGTGTGTCACTGCCGTCCCCGGAGGGCAGATAAGGCCCGCCCAA
AGGGTTCTGCTGGCGTCGGGCTTGGCGGCCCTGGGTCCGCCGTGGCCGGAGGCCCTA
GGAGCTGGTGTGCTGCCCGCCGGCCGGAGGGAGGGCAGGCCGGCCCCCACACTGTGCC
TGAGGGCCCGAACGGTCTCGCACCCGGCTGCCCTGCCCCAGTCAGGGCTTTAGAAGAGCTTTAC
TTGGGCCCGCCGCTCTGGCGCAACTGGAATGCAATACTACTTTATGTGCTGTGTT
TTTATTCTTGATACATTGATTTTACGTAAGTCCACATATACTCTATAAGAGCGTG
ACTTGTAATAAAGGGTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307
><subunit 1 of 1, 548 aa, 1 stop
><MW: 63198, pI: 8.10, NX(S/T): 4
MRLRNGTFLTLLFCFLCAFLSWSYAAALSGQKGDVVDVYQREFLALRDRLHAAEQESLKR SK
ELNLVLDEIKRAVSERQALRGDGDNRTWGRLTEDPRLKPWNGSHRVHLHLPTVFHHLPHLLA
KESSLQPAVRVGQGRTGVSVVMGIPSVRREVHSYLTDTLHSLISELSPQEKE DSVIVVLIAE
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLRESFGDPKERVRWRTKQNL D
YCFLMMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMF KSL
DLSLIVEFILEMFYRDKPIDWL LDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGTH
SSLAGKIQKLKDQDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDFFWAFTPAAGD
FIRFRFFQPLRLERFFF RSGNIEHPEDKLFNTSVEVLPFDNPQSDKEALQEGRATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAPGPLEALRLSITQTDSPVWVILSEIFLKKAD

Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515